RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.

Application Serial Number: *10/567,763*

Source: *IFWP*

Date Processed by STIC: *2/27/06*

ENTERED

IFWP

RAW SEQUENCE LISTING   DATE: 02/27/2006
PATENT APPLICATION: US/10/567,763   TIME: 14:42:07

        Input Set : A:\21864wo.ST25.txt
        Output Set: N:\CRF4\02272006\J567763.raw

      3 <110> APPLICANT: DSM IP Assets B.V.
      5 <120> TITLE OF INVENTION: Microbial production of L-ascorbic acid
      7 <130> FILE REFERENCE: 21864 WO
C--> 9 <140> CURRENT APPLICATION NUMBER: US/10/567,763
C--> 9 <141> CURRENT FILING DATE: 2006-02-10
      9 <150> PRIOR APPLICATION NUMBER: EP 03017677.0
     10 <151> PRIOR FILING DATE: 2003-08-14
     12 <160> NUMBER OF SEQ ID NOS: 31
     14 <170> SOFTWARE: PatentIn version 3.2
     16 <210> SEQ ID NO: 1
     17 <211> LENGTH: 2367
     18 <212> TYPE: DNA
     19 <213> ORGANISM: Gluconobacter oxydans N44-1
     21 <400> SEQUENCE: 1
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     24 gccttcctga tcatcgaagg cctccacctc atcatcctcg gcggctcgtg gttctacacc   120
     26 ctcgccggca tcgcgctggc ggccagcagc gtctacatga tccgtcgcaa catcctctcg   180
     28 acatggatcg ccctgggcct gcttgtggca acagccctgt ggtcgctcgc cgaagtcggc   240
     30 accagcttct ggcccagctt ctcccgcctg atcgtgttcc tgtgcgtcgc cctgatcgcg   300
     32 actctcatgg cgccctggct cagcggcccc ggccggcgct acttcacccg ccccgtcaca   360
     34 ggcgccacat ccggcgccct cggcgcgatc atcgtggctt tcctcgccgg catgttccgg   420
     36 gtccacccga ccatcgcccc gcaggacacc acccacccgc aggaaaccgc gtccaccgcc   480
     38 gactccgacc agccaggcca tgactggccc gcctatggcc gcacggcttc cggcacgcgc   540
     40 tacgccagct tcacgcagat caaccgcgac aatgtcagca agctccgcgt cgcctggacc   600
     42 taccgcaccg gcgacatggc gctgaacggc gccgagttcc agggcacccc catcaagatc   660
     44 ggcgacacgg tctatatctg ctcaccgcac aacatcgtct cggcccttga cccggacacc   720
     46 ggcacggaaa agtggaagtt cgacccccac gcccagacga agtctggca gcgctgccgc   780
     48 ggcgtcggct actggcatga cagcacggcc acggacgcca acgcgccctg cgcctcgcgc   840
     50 atcgtcctca ccacgatcga cgcccgcctc atcaccatcg acgcccgtac cggccaggcc   900
     52 tgcacggatt tcggaacgaa cggcaacgtc aatctcctga ccggcctcgg cccgacagct   960
     54 cccggctcgt actacccgac cgccgccccc ctcgtggcgg gtgacatcgt ggtcgtcggc 1020
     56 ggccgcatcg ccgataacga gcgcaccggc gagccctccg gcgtcgtccg cggctatgat 1080
     58 gtccgcaccg gcgcacaggt ctgggcctgg gacgccacca acccgcatcg cggcaccaca 1140
     60 cctctggccg aaggcgagat ctaccccgcc gaaacccca acatgtgggg caccgccagc 1200
     62 tacgacccga aactcaacct cgtcttcttc ccgctcggca accagacccc cgatttctgg 1260
     64 ggcggcgacc gcagcaaggc ctcagacgaa tacaacgacg ccttcgtcgc cgtggacgcc 1320
     66 aagaccggcg acgaacgctg gcacttccgc accgccaacc acgacctcgt ggactacgat 1380
     68 gccacggccc agcccatcct ctatgacatt ccggacggcc atggcggcac ccgcccggcg 1440
     70 atcatcgcca tgaccaagcg cggccagatc ttcgtgctcg accgccgcga cggcacccccg 1500
     72 atcgtccctg tggaaatgcg caaagtcccg caggacggcg caccggaaca ccagtacctc 1560
     74 gcccccgaac agccctattc cgccctctcc atcggaacag agcgcctgaa acccagcgac 1620
     76 atgtgggggtg gtacgatctt cgaccagctc ctgtgccgca tccagttcgc ctcctaccgc 1680
     78 tatgaaggcg agttcacccc cgtcaacgag aaacaggcca ccatcatcta tccgggctat 1740

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 80 tacggcggca tcaactgggg cggcggcgcc gtggatgaaa gcaccggaac gctgctggtc   1800
 82 aacgacatcc gcatggccca gtggggcaag ttcatgaagc aggaagaagc ccgtcgcagc   1860
 84 ggcttcaaac ccagctcgga aggcgaatat tccgaacaga aaggcacccc ctggggcgtc   1920
 86 gtccgctcga tgttcttctc ccccgccggt ctccctgcg tgaaaccgcc ctatggcacg   1980
 88 atgaacgcca tcgacctgcg cagcggcaag gtcaaatgga gcatgccgct ggcacgatc   2040
 90 caggacatgc cggtccacgg catggtccca ggcctcgcca tcccgctcgg aatgccgacc   2100
 92 atgagcggcc cgctggccac ccataccggc ctggtgttct ctccggcac gctcgacaac   2160
 94 tatgtccgcg cgctcaacac cgacaccggc gaagtcgtct ggaaagcccg tctccccgtc   2220
 96 gcctcacagg ccgctccgat gagctacatg tccgacaaga ccggcaaaca gtacatcgtc   2280
 98 gtcaccgcag cggcctgac ccgctccggc gtcgacaaaa accgcggcga ctacgtcatc   2340
100 gcctacgccc tgccctccga agaataa                                        2367
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104 <211> LENGTH: 788
105 <212> TYPE: PRT
106 <213> ORGANISM: Gluconobacter oxydans N44-1
108 <400> SEQUENCE: 2
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114 Ala Leu Met Ala Ala Phe Leu Ile Ile Glu Gly Leu His Leu Ile Ile
115             20·                  25                  30
118 Leu Gly Gly Ser Trp Phe Tyr Thr Leu Ala Gly Ile Ala Leu Ala Ala
119         35                  40                  45
122 Ser Ser Val Tyr Met Ile Arg Arg Asn Ile Leu Ser Thr Trp Ile Ala
123     50                  55                  60
126 Leu Gly Leu Leu Val Ala Thr Ala Leu Trp Ser Leu Ala Glu Val Gly
127 65                  70                  75                  80
130 Thr Ser Phe Trp Pro Ser Phe Ser Arg Leu Ile Val Phe Leu Cys Val
131             85                  90                  95
134 Ala Leu Ile Ala Thr Leu Met Ala Pro Trp Leu Ser Gly Pro Gly Arg
135             100                 105                 110
138 Arg Tyr Phe Thr Arg Pro Val Thr Gly Ala Thr Ser Gly Ala Leu Gly
139         115                 120                 125
142 Ala Ile Ile Val Ala Phe Leu Ala Gly Met Phe Arg Val His Pro Thr
143     130                 135                 140
146 Ile Ala Pro Gln Asp Thr Thr His Pro Gln Glu Thr Ala Ser Thr Ala
147 145                 150                 155                 160
150 Asp Ser Asp Gln Pro Gly His Asp Trp Pro Ala Tyr Gly Arg Thr Ala
151             165                 170                 175
154 Ser Gly Thr Arg Tyr Ala Ser Phe Thr Gln Ile Asn Arg Asp Asn Val
155             180                 185                 190
158 Ser Lys Leu Arg Val Ala Trp Thr Tyr Arg Thr Gly Asp Met Ala Leu
159         195                 200                 205
162 Asn Gly Ala Glu Phe Gln Gly Thr Pro Ile Lys Ile Gly Asp Thr Val
163     210                 215                 220
166 Tyr Ile Cys Ser Pro His Asn Ile Val Ser Ala Leu Asp Pro Asp Thr
167 225                 230                 235                 240
170 Gly Thr Glu Lys Trp Lys Phe Asp Pro His Ala Gln Thr Lys Val Trp
171             245                 250                 255
174 Gln Arg Cys Arg Gly Val Gly Tyr Trp His Asp Ser Thr Ala Thr Asp
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175             260                 265                 270
178 Ala Asn Ala Pro Cys Ala Ser Arg Ile Val Leu Thr Thr Ile Asp Ala
179         275                 280                 285
182 Arg Leu Ile Thr Ile Asp Ala Arg Thr Gly Gln Ala Cys Thr Asp Phe
183     290                 295                 300
186 Gly Thr Asn Gly Asn Val Asn Leu Leu Thr Gly Leu Gly Pro Thr Ala
187 305                 310                 315                 320
190 Pro Gly Ser Tyr Tyr Pro Thr Ala Ala Pro Leu Val Ala Gly Asp Ile
191             325                 330                 335
194 Val Val Val Gly Gly Arg Ile Ala Asp Asn Glu Arg Thr Gly Glu Pro
195         340                 345                 350
198 Ser Gly Val Val Arg Gly Tyr Asp Val Arg Thr Gly Ala Gln Val Trp
199     355                 360                 365
202 Ala Trp Asp Ala Thr Asn Pro His Arg Gly Thr Thr Pro Leu Ala Glu
203     370                 375                 380
206 Gly Glu Ile Tyr Pro Ala Glu Thr Pro Asn Met Trp Gly Thr Ala Ser
207 385                 390                 395                 400
210 Tyr Asp Pro Lys Leu Asn Leu Val Phe Phe Pro Leu Gly Asn Gln Thr
211             405                 410                 415
214 Pro Asp Phe Trp Gly Gly Asp Arg Ser Lys Ala Ser Asp Glu Tyr Asn
215         420                 425                 430
218 Asp Ala Phe Val Ala Val Asp Ala Lys Thr Gly Asp Glu Arg Trp His
219     435                 440                 445
222 Phe Arg Thr Ala Asn His Asp Leu Val Asp Tyr Asp Ala Thr Ala Gln
223     450                 455                 460
226 Pro Ile Leu Tyr Asp Ile Pro Asp Gly His Gly Gly Thr Arg Pro Ala
227 465                 470                 475                 480
230 Ile Ile Ala Met Thr Lys Arg Gly Gln Ile Phe Val Leu Asp Arg Arg
231             485                 490                 495
234 Asp Gly Thr Pro Ile Val Pro Val Glu Met Arg Lys Val Pro Gln Asp
235         500                 505                 510
238 Gly Ala Pro Glu His Gln Tyr Leu Ala Pro Glu Gln Pro Tyr Ser Ala
239     515                 520                 525
242 Leu Ser Ile Gly Thr Glu Arg Leu Lys Pro Ser Asp Met Trp Gly Gly
243     530                 535                 540
246 Thr Ile Phe Asp Gln Leu Leu Cys Arg Ile Gln Phe Ala Ser Tyr Arg
247 545             550                 555                 560
250 Tyr Glu Gly Glu Phe Thr Pro Val Asn Glu Lys Gln Ala Thr Ile Ile
251             565                 570                 575
254 Tyr Pro Gly Tyr Tyr Gly Gly Ile Asn Trp Gly Gly Gly Ala Val Asp
255         580                 585                 590
258 Glu Ser Thr Gly Thr Leu Leu Val Asn Asp Ile Arg Met Ala Gln Trp
259     595                 600                 605
262 Gly Lys Phe Met Lys Gln Glu Glu Ala Arg Arg Ser Gly Phe Lys Pro
263     610                 615                 620
266 Ser Ser Glu Gly Glu Tyr Ser Glu Gln Lys Gly Thr Pro Trp Gly Val
267 625             630                 635                 640
270 Val Arg Ser Met Phe Phe Ser Pro Ala Gly Leu Pro Cys Val Lys Pro
271             645                 650                 655
```

```
274 Pro Tyr Gly Thr Met Asn Ala Ile Asp Leu Arg Ser Gly Lys Val Lys
275             660             665             670
278 Trp Ser Met Pro Leu Gly Thr Ile Gln Asp Met Pro Val His Gly Met
279         675             680             685
282 Val Pro Gly Leu Ala Ile Pro Leu Gly Met Pro Thr Met Ser Gly Pro
283     690             695             700
286 Leu Ala Thr His Thr Gly Leu Val Phe Phe Ser Gly Thr Leu Asp Asn
287 705         710             715             720
290 Tyr Val Arg Ala Leu Asn Thr Asp Thr Gly Glu Val Val Trp Lys Ala
291             725             730             735
294 Arg Leu Pro Val Ala Ser Gln Ala Ala Pro Met Ser Tyr Met Ser Asp
295         740             745             750
298 Lys Thr Gly Lys Gln Tyr Ile Val Val Thr Ala Gly Gly Leu Thr Arg
299         755             760             765
302 Ser Gly Val Asp Lys Asn Arg Gly Asp Tyr Val Ile Ala Tyr Ala Leu
303     770             775             780
306 Pro Ser Glu Glu
307 785
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311 <211> LENGTH: 20
312 <212> TYPE: DNA
313 <213> ORGANISM: Artificial
315 <220> FEATURE:
316 <223> OTHER INFORMATION: Primer
318 <400> SEQUENCE: 3
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322 <210> SEQ ID NO: 4
323 <211> LENGTH: 20
324 <212> TYPE: DNA
325 <213> ORGANISM: Artificial
327 <220> FEATURE:
328 <223> OTHER INFORMATION: Primer
330 <400> SEQUENCE: 4
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334 <210> SEQ ID NO: 5
335 <211> LENGTH: 30
336 <212> TYPE: DNA
337 <213> ORGANISM: Artificial
339 <220> FEATURE:
340 <223> OTHER INFORMATION: Primer
342 <400> SEQUENCE: 5
343 atgaacagcg gcccccgcac gctctccatg                             30
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347 <211> LENGTH: 30
348 <212> TYPE: DNA
349 <213> ORGANISM: Artificial
351 <220> FEATURE:
352 <223> OTHER INFORMATION: Primer
354 <400> SEQUENCE: 6
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358 <210> SEQ ID NO: 7
359 <211> LENGTH: 30
360 <212> TYPE: DNA
361 <213> ORGANISM: Artificial
363 <220> FEATURE:
364 <223> OTHER INFORMATION: Primer
366 <400> SEQUENCE: 7
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370 <210> SEQ ID NO: 8
371 <211> LENGTH: 30
372 <212> TYPE: DNA
373 <213> ORGANISM: Artificial
375 <220> FEATURE:
376 <223> OTHER INFORMATION: Primer
378 <400> SEQUENCE: 8
379 ttcttcggag ggcagggcgt aggcgatgac                                    30
382 <210> SEQ ID NO: 9
383 <211> LENGTH: 30
384 <212> TYPE: DNA
385 <213> ORGANISM: Artificial
387 <220> FEATURE:
388 <223> OTHER INFORMATION: Primer
390 <400> SEQUENCE: 9
391 cgggactttg cgcatttcca cagggacgat                                    30
394 <210> SEQ ID NO: 10
395 <211> LENGTH: 30
396 <212> TYPE: DNA
397 <213> ORGANISM: Artificial
399 <220> FEATURE:
400 <223> OTHER INFORMATION: Primer
402 <400> SEQUENCE: 10
403 agcccatcct ctatgacatt ccggacggcc                                    30
406 <210> SEQ ID NO: 11
407 <211> LENGTH: 771
408 <212> TYPE: DNA
409 <213> ORGANISM: Gluconobacter oxydans IFO 3292
411 <400> SEQUENCE: 11
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414 cggcaccccg atcgtccccg tggaaatgcg caaagtcccc caggacggcg caccggaaca   120
416 ccagtacctc gcccccgaac agccctattc cgccctctcc atcggaacag agcgcctgaa   180
418 acccagcgat atgtggggcg gcacgatctt cgaccagctc ctgtgccgca tccagttcgc   240
420 ctcctaccgc tatgaaggcg agttcacccc cgtcaacgag aagcaggcca ccatcatcta   300
422 tccgggctat tacggcggca tcaactgggg cggcggcgcc gtggatgaaa gcaccggaac   360
424 gctgctggtc aacgacatcc gcatggccca gtggggcaag ttcatgaagc aagaagaagc   420
426 ccgccgcagc ggcttcaaac ccagctcgga aggcgaatat tccgaacaga aaggcacccc   480
428 ctggggcgtc gtccgctcga tgttcttctc ccccgccggt ctccctgcg tgaaaccgcc   540
430 ctatggcacg atgaacgcca tcgacctgcg cagcggcaag gtcaaatgga gcatgccgct   600
432 tggcacgatc caggacatgc cggtccacgg catggtcccc ggcctcgcca tcccgctcgg   660
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RAW SEQUENCE LISTING ERROR SUMMARY   DATE: 02/27/2006
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<u>**Please Note:**</u>
Use of n and/or Xaa have been detected in the Sequence Listing. Please review the
Sequence Listing to ensure that a corresponding explanation is presented in the <220>
to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:13; N Pos. 123
Seq#:19; N Pos. 123

<u>**Invalid <213> Response:**</u>
Use of "Artificial" only as "<213> Organism" response is incomplete,
per 1.823(b) of New Sequence Rules. Valid response is Artificial Sequence.

Seq#:3,4,5,6,7,8,9,10,23,24,25,28,29,30,31

VERIFICATION SUMMARY   DATE: 02/27/2006
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```
L:9 M:270 C: Current Application Number differs, Replaced Current Application No
L:9 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:526 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:13 after pos.:120
L:810 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:19 after pos.:120
```